

### **REMARKS**

With this response, Applicants have canceled claims 12-29, 31-32, 36, and 38-40, amended claims 1-3, 5, 30, 34, 35, and 41, and added new claims 43-51. Upon entry of this Amendment, claims 1-11, 30, 33-35, 37, and 41-51 are pending.

Support for the amended and newly added claims 43-51 can be found, for example, in the original claims and in the specification, and sequence listing as filed. Accordingly, no new matter is added by these amendments.

#### **Restriction Requirement**

In the Office communication dated August 2, 2006, requiring restriction and election under 35 U.S.C. § 121, the Examiner requests restriction to one of the following:

- I. Claims 1-11, 30, 33-35, 37, 41, and 42, drawn to an antibody;
- II. Claims 12-23, 32, and 36, drawn to methods of treatment comprising administering the antibody;
- III. Claims 24-29 and 38-40, drawn to nucleic acids encoding an antibody, vectors and host cells comprising the nucleic acid, and methods of recombinantly expressing the antibody; and
- IV. Claim 31, drawn to a method of identifying inhibitors.

Applicants provisionally elect to prosecute Group I, claims 1-11, 30, 33-35, 37, 41, 42, and newly added claims 43-51, drawn to an antibody.

The Examiner has further required an election between the following antibody species: SEQ ID NO:2, 4, 6, 8, 10, 12, 14, 16, 18, 20, 22, 24, 26, 28, 30, 31, 32, 33, 34, 35, 36, 37, 38, 39, 40, 41, 42, 43, 44, 45, 46, 47; and 48. Applicants provisionally elect to prosecute SEQ ID NO:14, with traverse.

Applicants traverse the election requirement on the basis that a structural and functional relationship exists between the species, and as such, the claims include sufficiently few species that a search and examination would not impose a serious burden on the examiner. Original claim 1 is directed to an antibody comprising sequences that relate to one of three antibodies (Myo29, Myo28, and Myo22). For example, the amino acid sequences of SEQ ID NOs:14, 16, 18, 26, 28, and 30-36 relate to the antibody Myo29, amino acid sequences of SEQ ID NOs: 8, 10, 12, 20, 22, 24, and 37-42 relate to the antibody Myo28, and amino acid sequences of SEQ ID NOs: 2, 4, 6, and 43-48 relate to the antibody Myo22. See Table 1 on page 21 of the specification. With this response, the claims are amended to comprise only the amino acid sequences relating to Myo29. As described in more detail below, the sequences recited in the amended claims are both structurally and functionally related. Accordingly, a search should not pose any burden to the Examiner.

The claimed sequences are functionally related, because when expressed, they share the functional property of binding to GDF-8 or BMP-11. Moreover, all of the sequences recited in the amended claims are structurally related to SEQ ID NO:14. As depicted in Table 1 below, SEQ ID NO:14 is the amino acid sequence for a scFV relating to Myo29. As is well known to those of skill in the art, and described in the specification on page 18, lines 3-7, a scFV comprises a variable heavy ( $V_H$ ), and a variable light ( $V_L$ ) chain linked via a polypeptide linker. Here, the scFV for Myo29 (SEQ ID NO:14) comprises a  $V_H$  (SEQ ID NO:16), and a  $V_L$  (SEQ ID NO:18), connected via a polypeptide linker. As is shown in the table, SEQ ID NO:16 corresponds to amino

acids 1 to 117 of SEQ ID NO:14, and SEQ ID NO:18 corresponds to amino acids 135-239 of SEQ ID NO:14. The V<sub>H</sub> of Myo29 comprises three CDRs (designated "H1", "H2", and "H3"), and the V<sub>L</sub> of Myo29 comprises three CDRs (designated "L1", "L2", and "L3"), which correspond to SEQ ID NOs:31-33, and SEQ ID NOs:34-36, respectively. Table 1 shows the relationship of these CDRs to SEQ ID NO:14.

**TABLE 1**

|                                  | <b>Myo29</b> | <b>Relationship to SEQ ID NO: 14</b>  |
|----------------------------------|--------------|---|
| <b>AA* sequence of scFv</b>      | SEQ ID NO:14 |   |
| <b>AA sequence of VH</b>         | SEQ ID NO:16 | AA 1 to 117 of SEQ ID NO:14   |
| <b>AA sequence of VL</b>         | SEQ ID NO:18 | AA 135 to 239 of SEQ ID NO:14   |
| <b>Germlined AA seq. of scFv</b> | SEQ ID NO:26 | Corresponds to AA 1 to 249 of SEQ ID NO:14, but AA 153, 172, 173, 193, and 220 differ   |
| <b>Germlined AA seq. of VH</b>   | SEQ ID NO:28 | AA 1 to 117 of SEQ ID NO:14   |
| <b>Germlined AA seq. of VL</b>   | SEQ ID NO:30 | Corresponds to AA 135 to 239 of SEQ ID NO:14, but AA 153, 172, 173, 193, and 220 differ |
| <b>AA sequence of H1</b>         | SEQ ID NO:31 | AA 31 to 35 of SEQ ID NO:14   |
| <b>AA sequence of H2</b>         | SEQ ID NO:32 | AA 50 to 66 of SEQ ID NO:14   |
| <b>AA sequence of H3</b>         | SEQ ID NO:33 | AA 99 to 106 of SEQ ID NO:14  |
| <b>AA sequence of L1</b>         | SEQ ID NO:34 | AA 157 to 167 of SEQ ID NO:14   |
| <b>AA sequence of L2</b>         | SEQ ID NO:35 | AA 183 to 189 of SEQ ID NO:14   |
| <b>AA sequence of L3</b>         | SEQ ID NO:36 | AA 222 to 228 of SEQ ID NO:14   |

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\* AA = amino acid

SEQ ID NO:26 is the germlined version of SEQ ID NO:14, and is thus structurally and functionally related to Myo29. As is shown on the attached sequence alignment, SEQ ID NO:14 and SEQ ID NO:26 differ by only 5 amino acids, none of which fall within the antigen binding domains, and as such, do not alter the functional property of binding to GDF-8 or BMP-11.

Notwithstanding the structural and functional relationship that exists between the claimed amino acid sequences, Applicants note that the M.P.E.P. requires the examination of a reasonable number of sequences, and states that up to ten independent and distinct sequences should be examined without restriction. Manual of Patent Examining Procedure, § 803.04.

Conclusion

In view of the foregoing amendments and remarks, Applicants respectfully request reconsideration and reexamination of this application and the timely allowance of the pending claims.

Please grant any extensions of time required to enter this response and charge any additional required fees to our deposit account 06-0916.

Respectfully submitted,

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GARRETT & DUNNER, L.L.P.

Dated: September 29, 2006

By: J. Amelia Feulner  
J. Amelia Feulner  
Reg. No. 58,039

## ATTACHMENT

### SEQUENCE ALIGNMENT OF SEQ ID NO:14 AND SEQ ID NO:26

Score = 508 bits (1309), Expect = 1e-142

Identities = 244/249 (97%), Positives = 246/249 (98%), Gaps = 0/249 (0%)

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Query 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGIINPSGGSTSY 60
Sbjct 1 QVQLVQSGAEVKKPGASVKVSCKASGYTFTSYMHVVRQAPGQGLEWMGIINPSGGSTSY 60

Query 61 AQKFQGRVTMTTRDTSTSTVYMESSLRSEDVAVYYCARDENWGFDPPWGQGLTVTVSSGGG 120
Sbjct 61 AQKFQGRVTMTTRDTSTSTVYMESSLRSEDVAVYYCARDENWGFDPPWGQGLTVTVSSGGG 120

Query 121 GSGGGGSGGGGSALSYELTQPPSVSVSPGQTASITCSGHALGDKFVSWYQQKPGQSPVLV 180
Sbjct 121 GSGGGGSGGGGSALSYELTQPPSVSVSPGQTA+ITCSGHALGDKFVSWYQQ--GQSPVLV 180

Query 181 IYDDTQRPISGIPERFSGSNSGNTATLTISGTQAMDEADYYCQAWDSSFVFGGGTKVTVLG 240
Sbjct 181 IYDDTQRPISGIPERFSGSNSGNTATLTISGTQAMDEADY+CQAWDSSFVFGGGTKVTVLG 240

Query 241 AAHHHHHHH 249
Sbjct 241 AAHHHHHHH 249
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Query = SEQ ID NO:26

Sbjct = SEQ ID NO:14